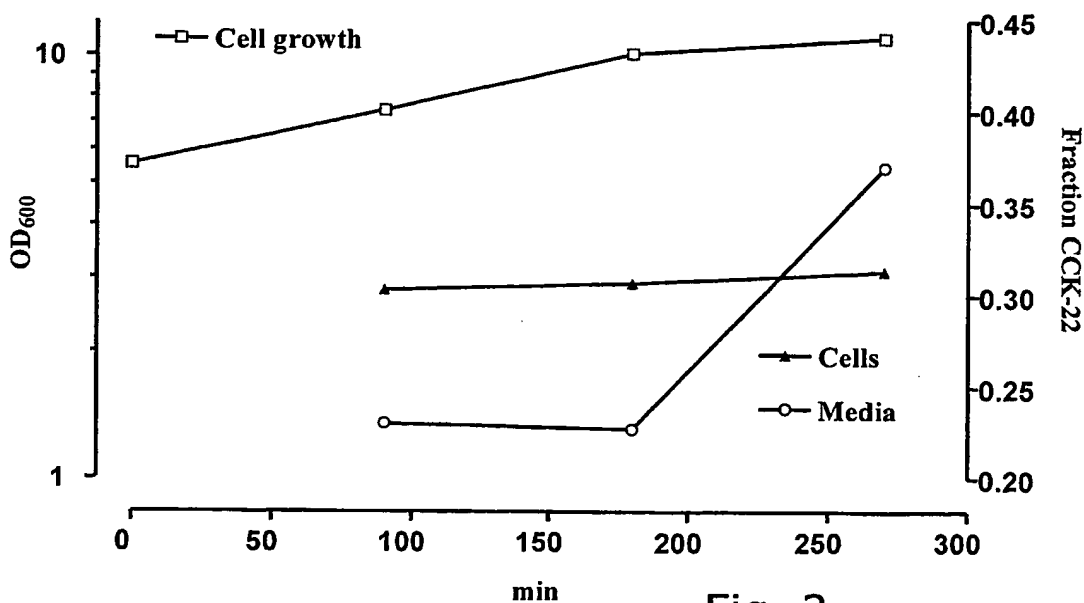
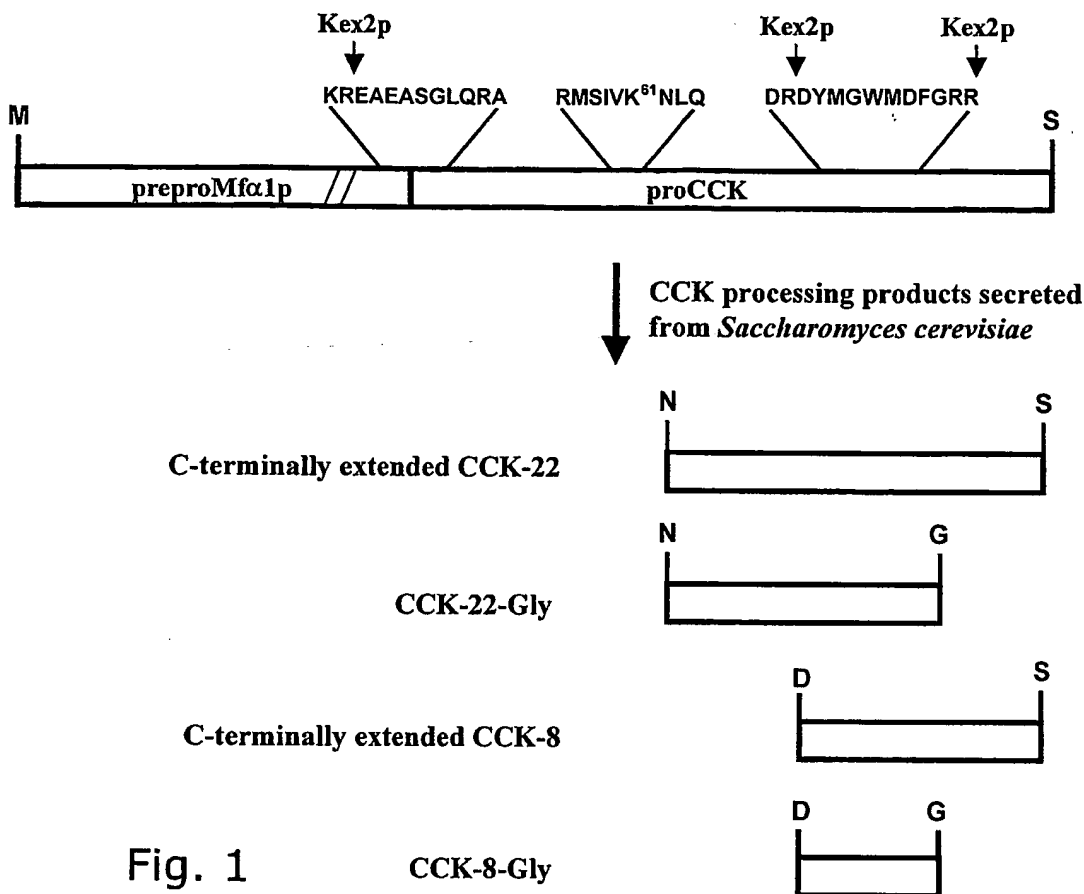


1/17



2/17

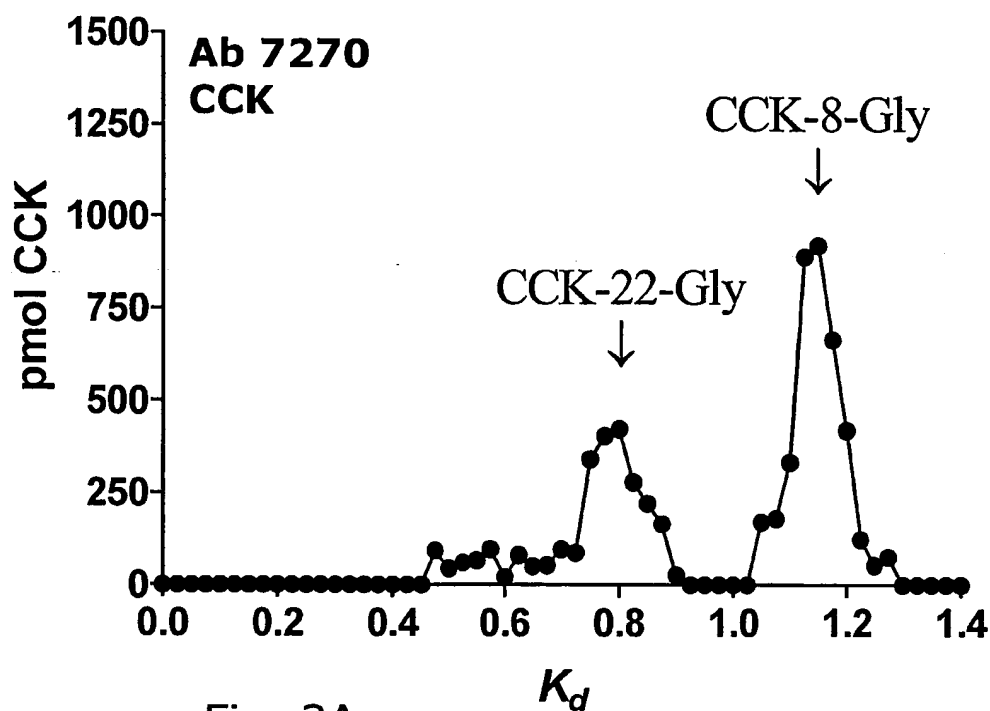


Fig. 3A

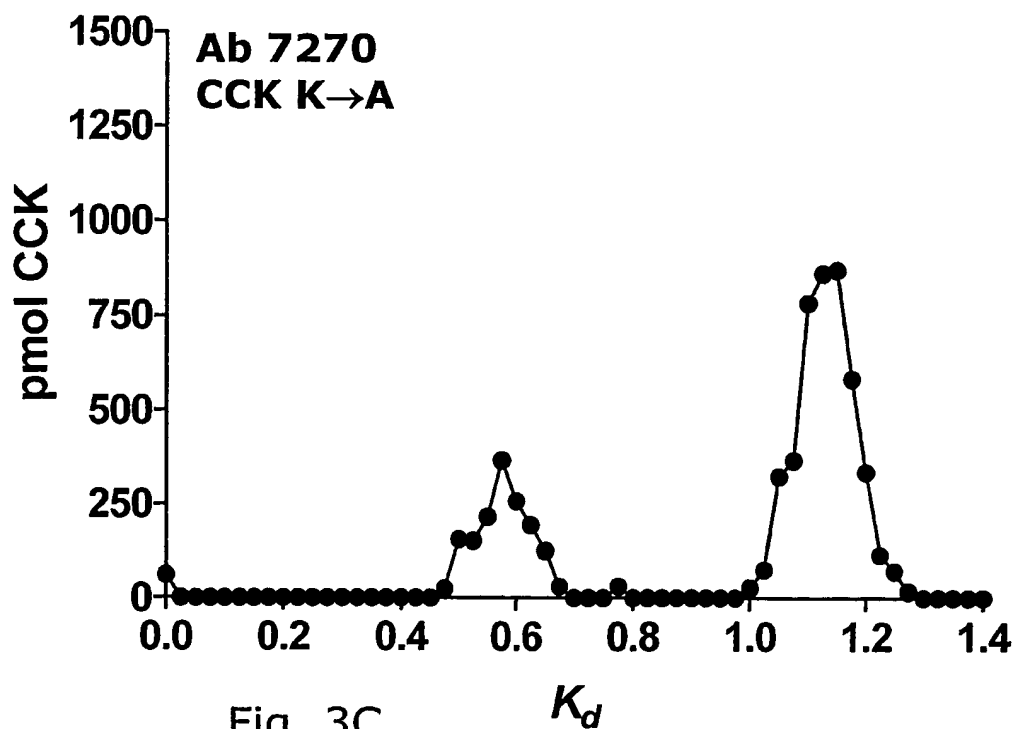


Fig. 3C

3/17

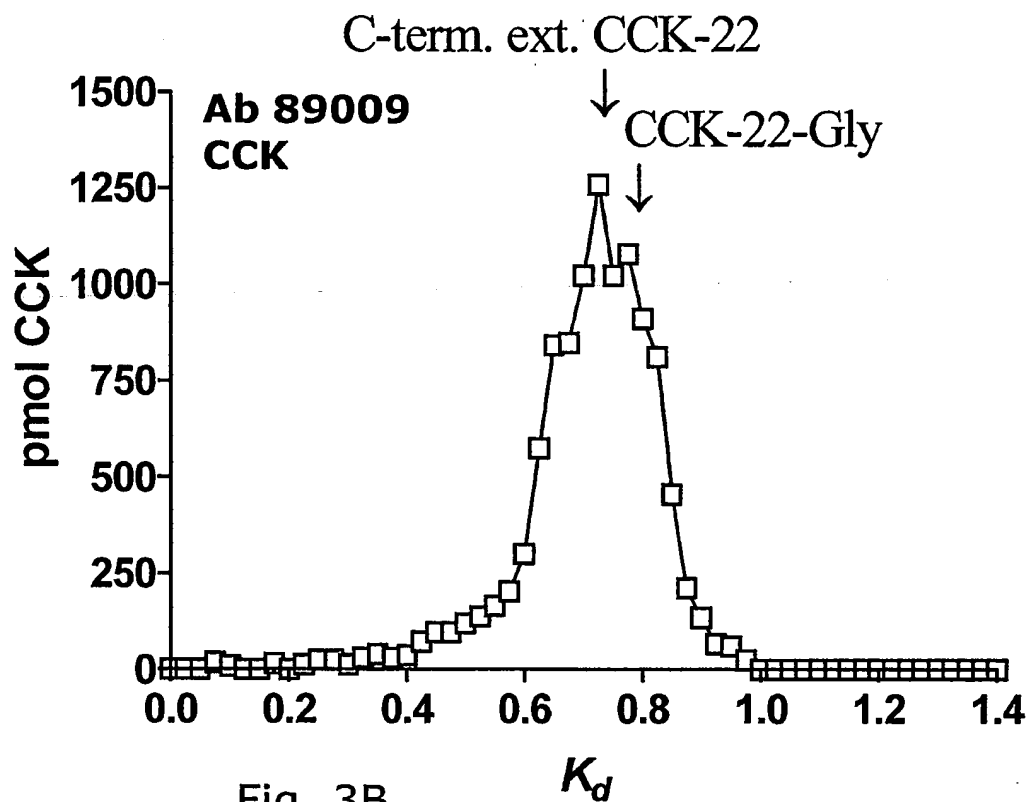


Fig. 3B

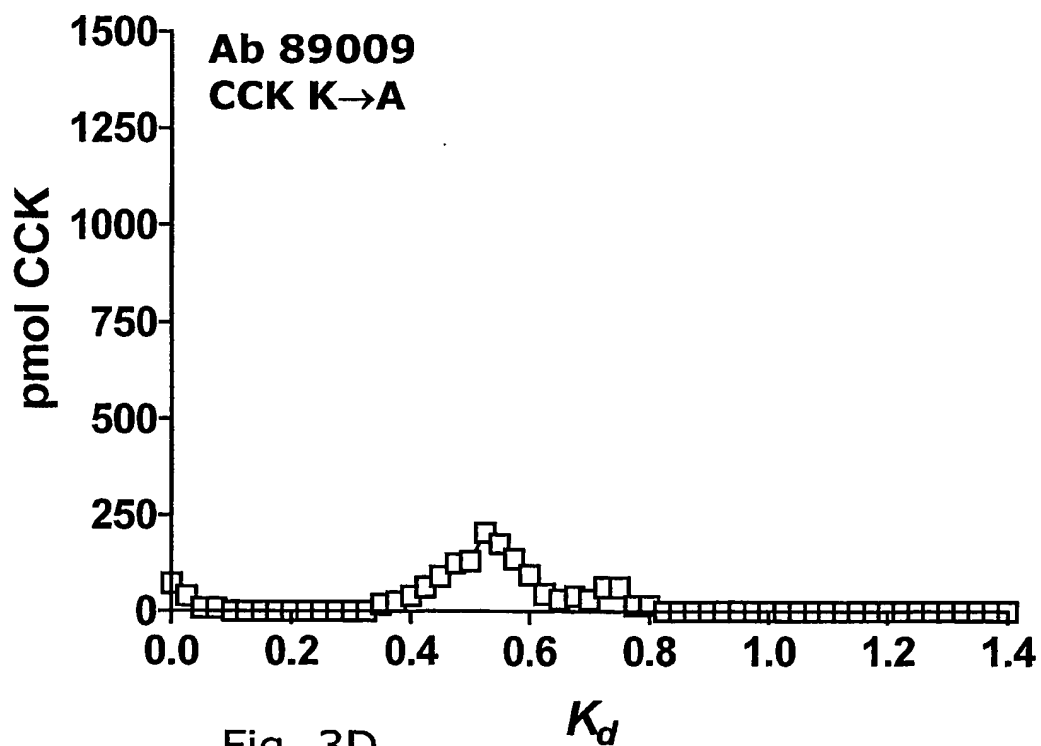
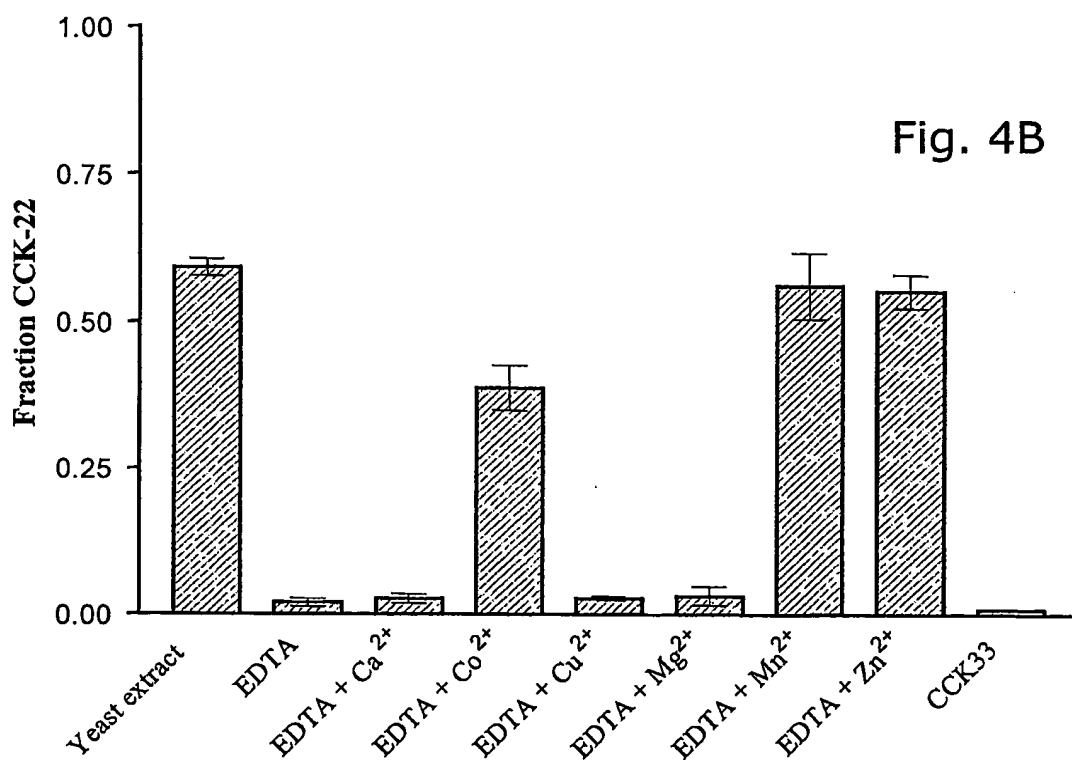
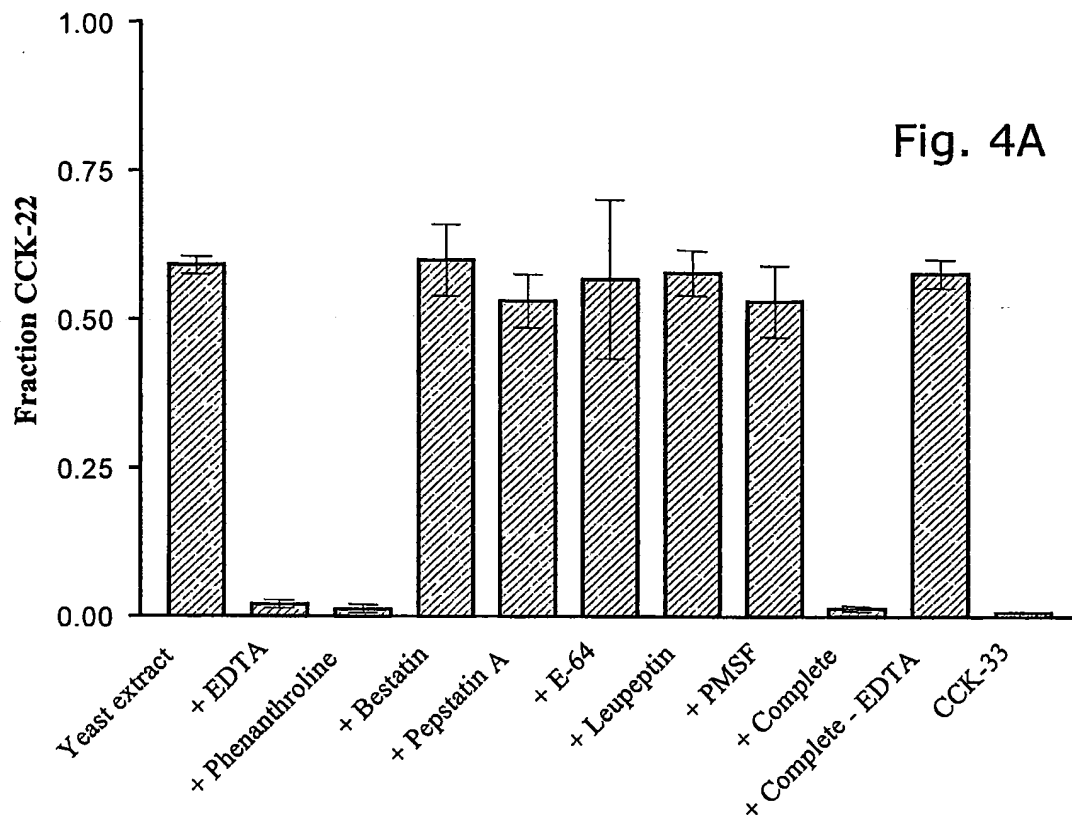


Fig. 3D

4/17



5/17

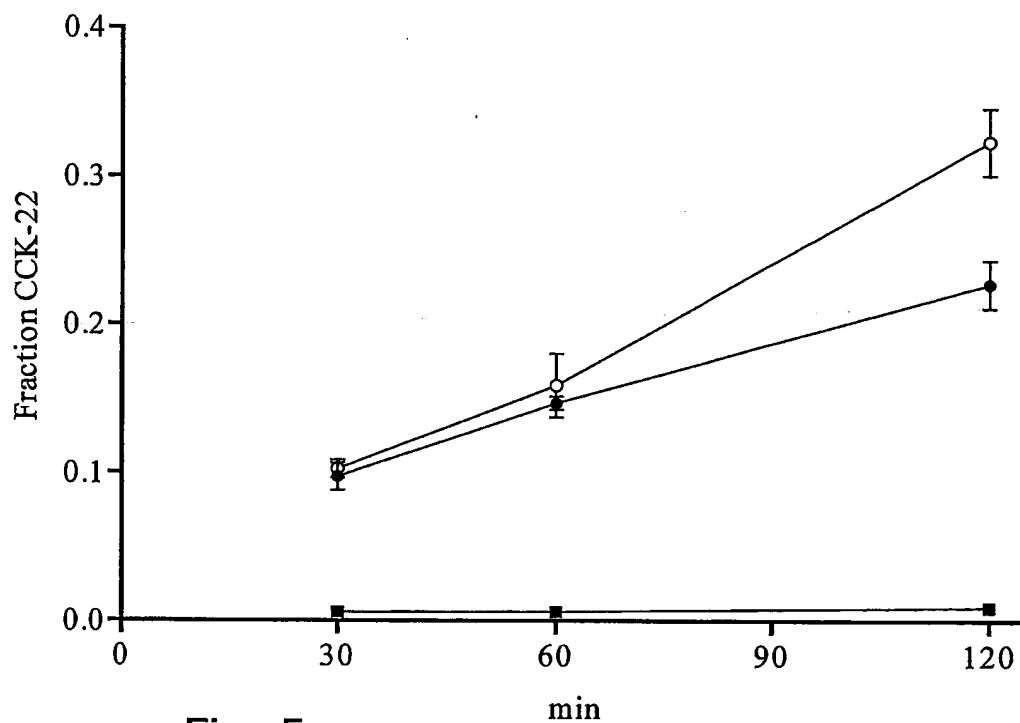


Fig. 5

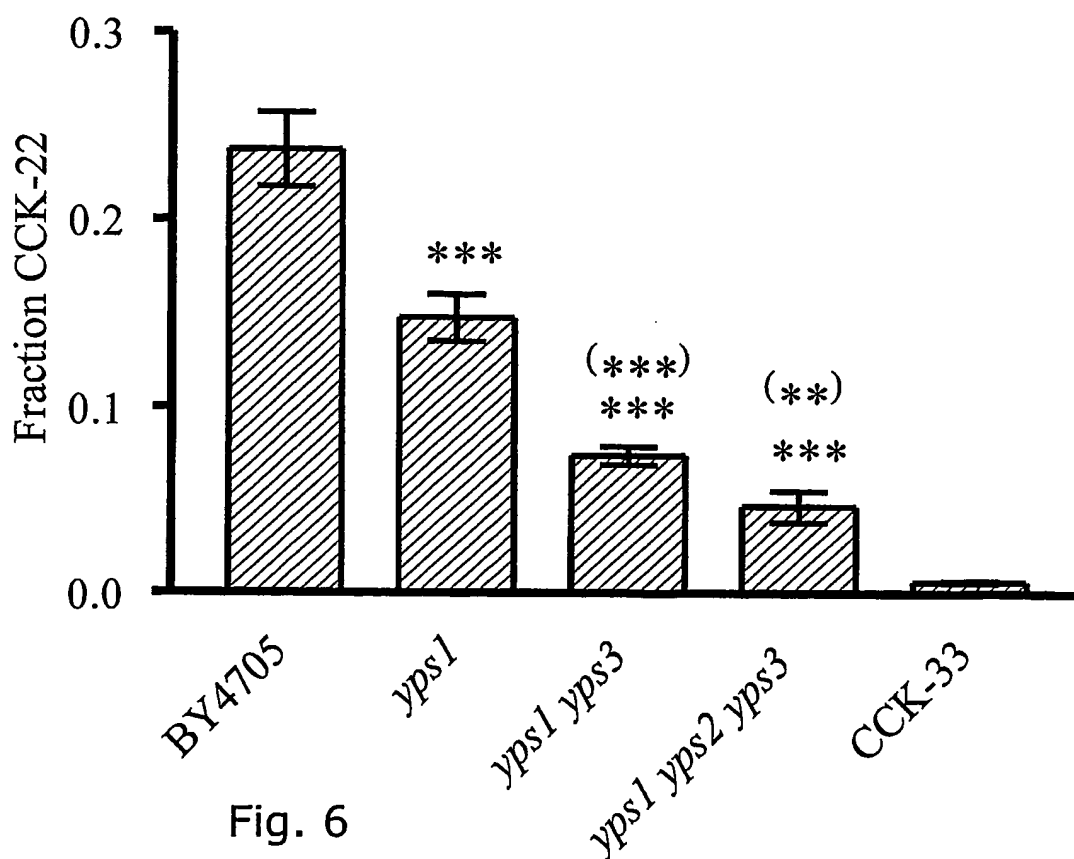
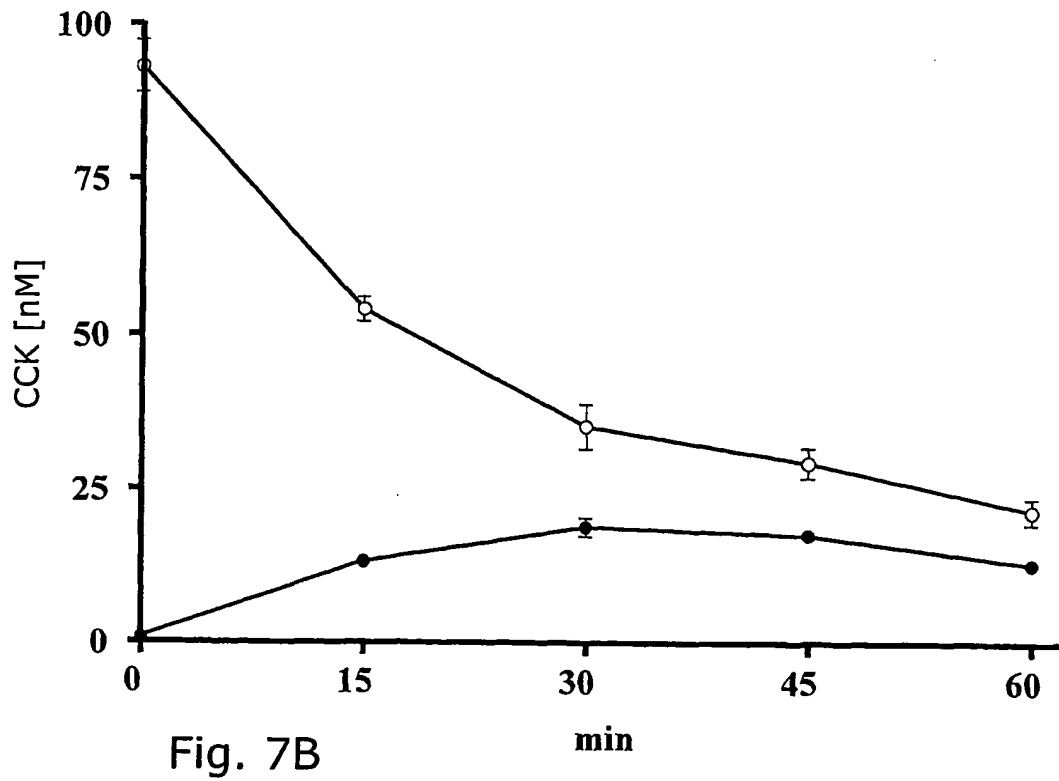
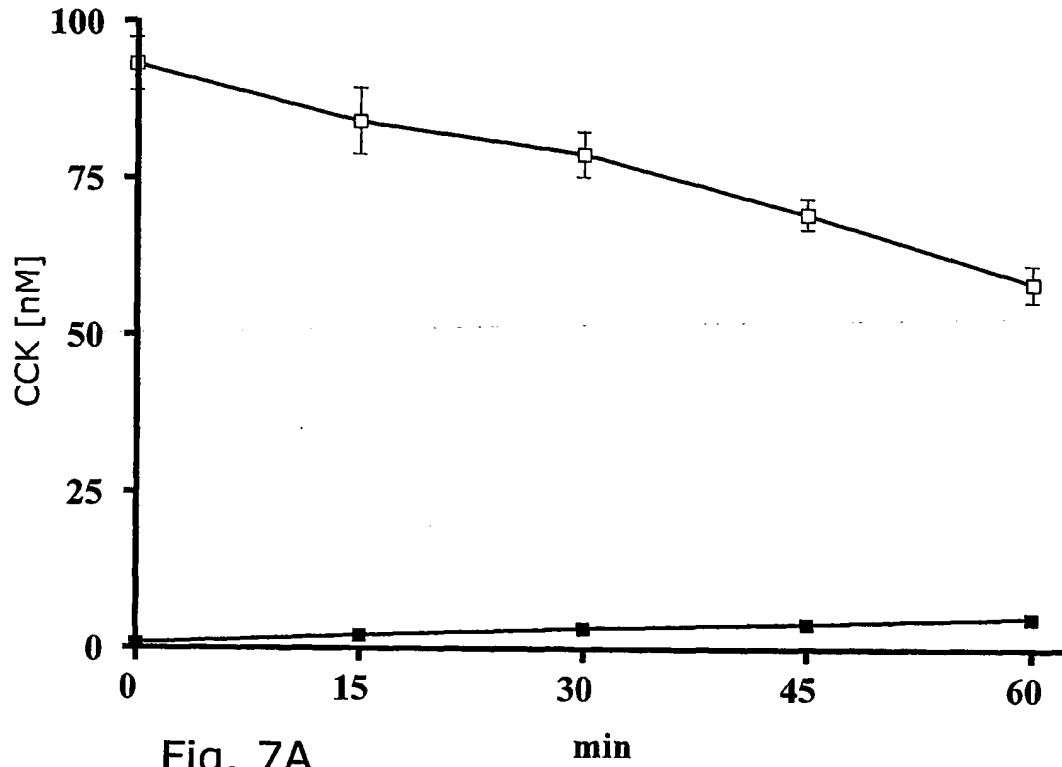


Fig. 6

005 2004 02 27 067

6/17



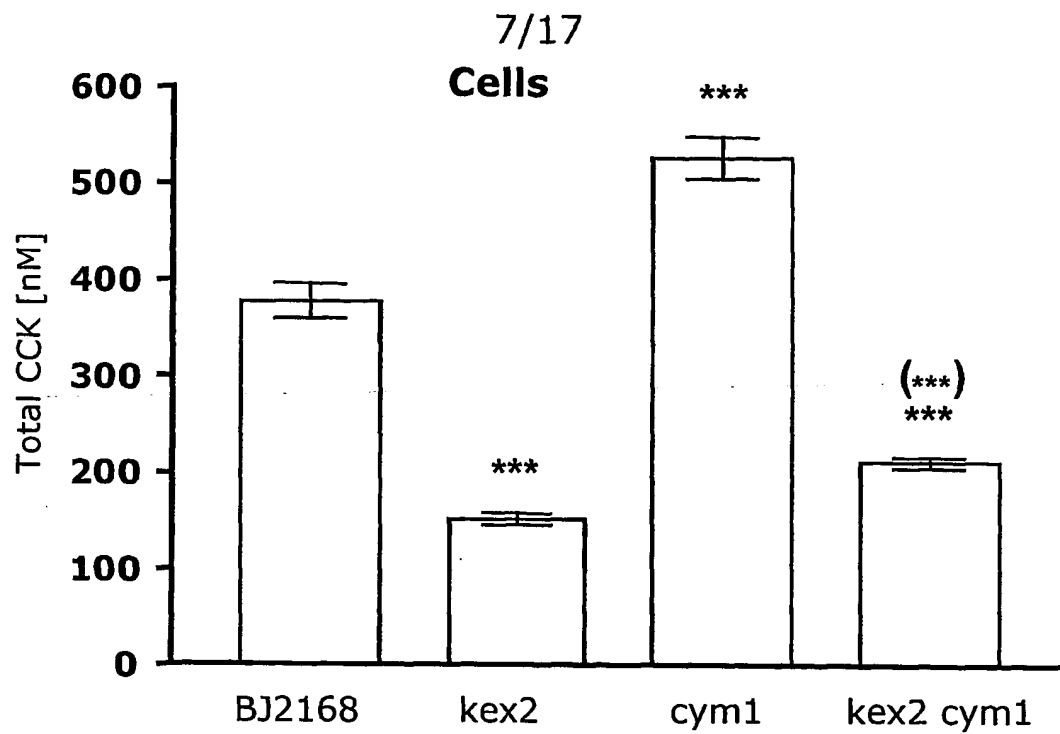


Fig. 8A

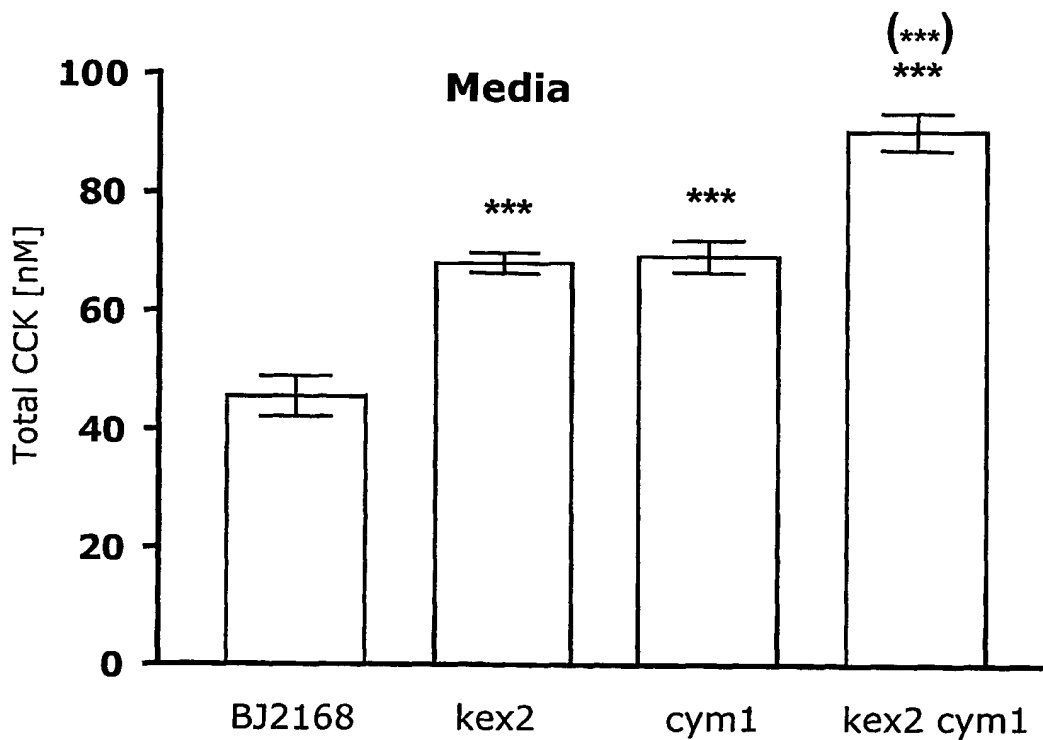


Fig. 8B

8/17

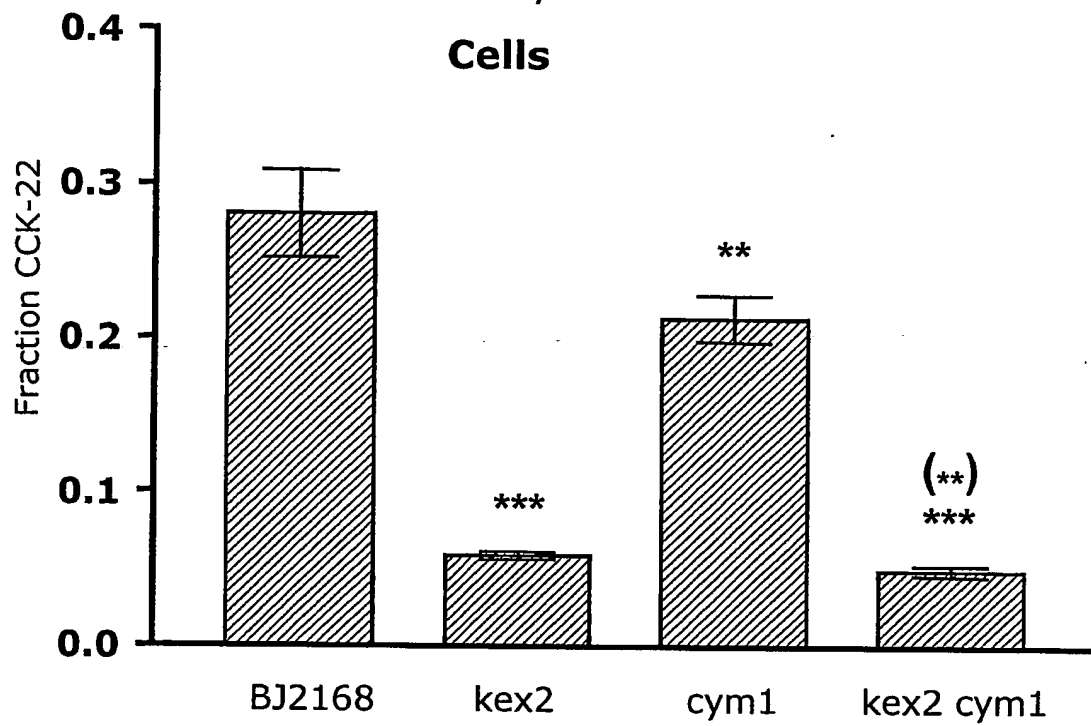


Fig. 8C

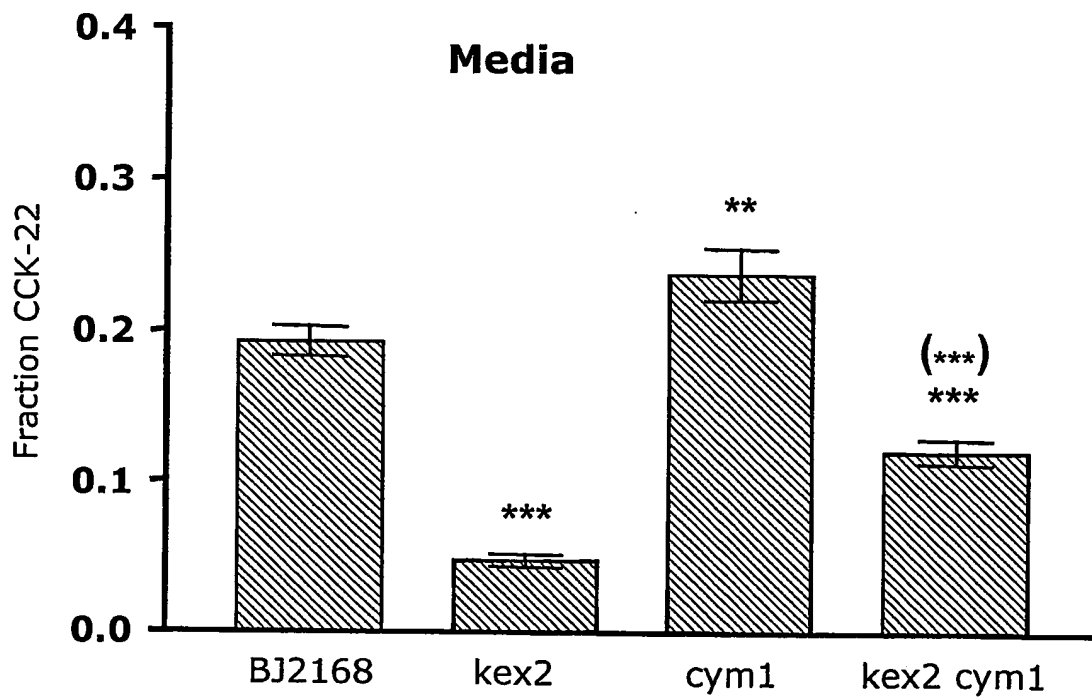


Fig. 8D

9/17

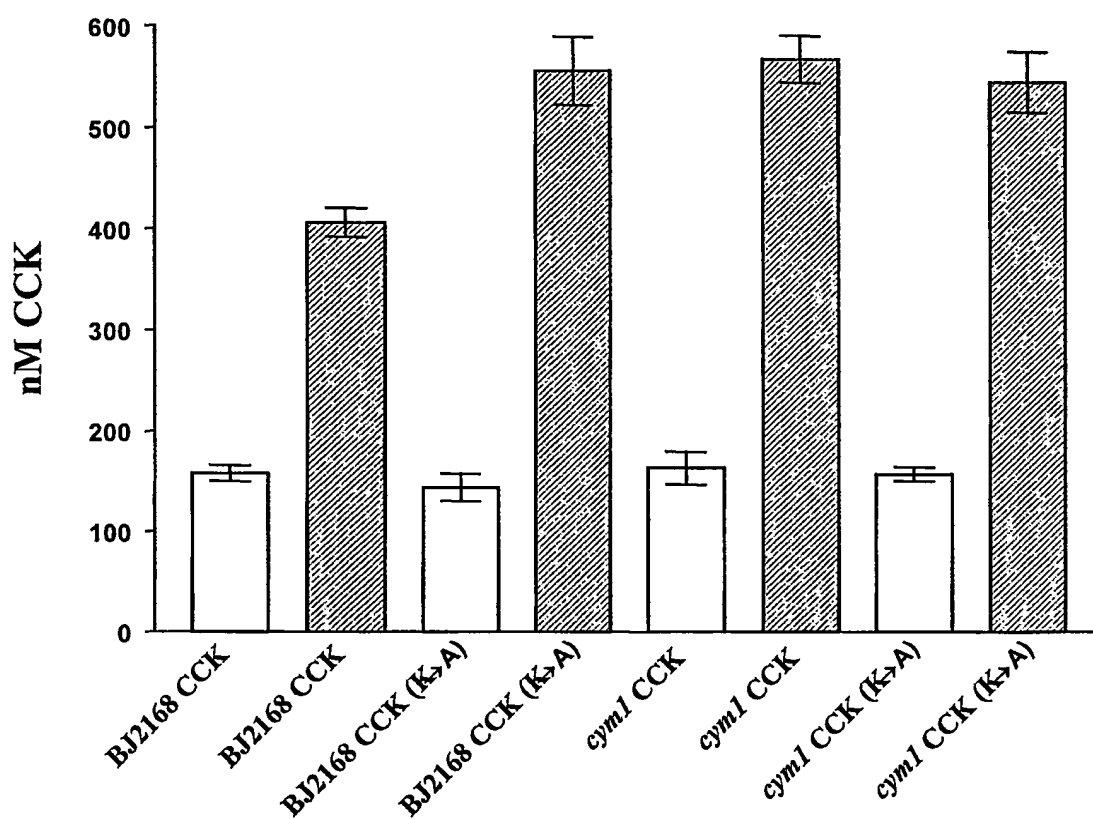
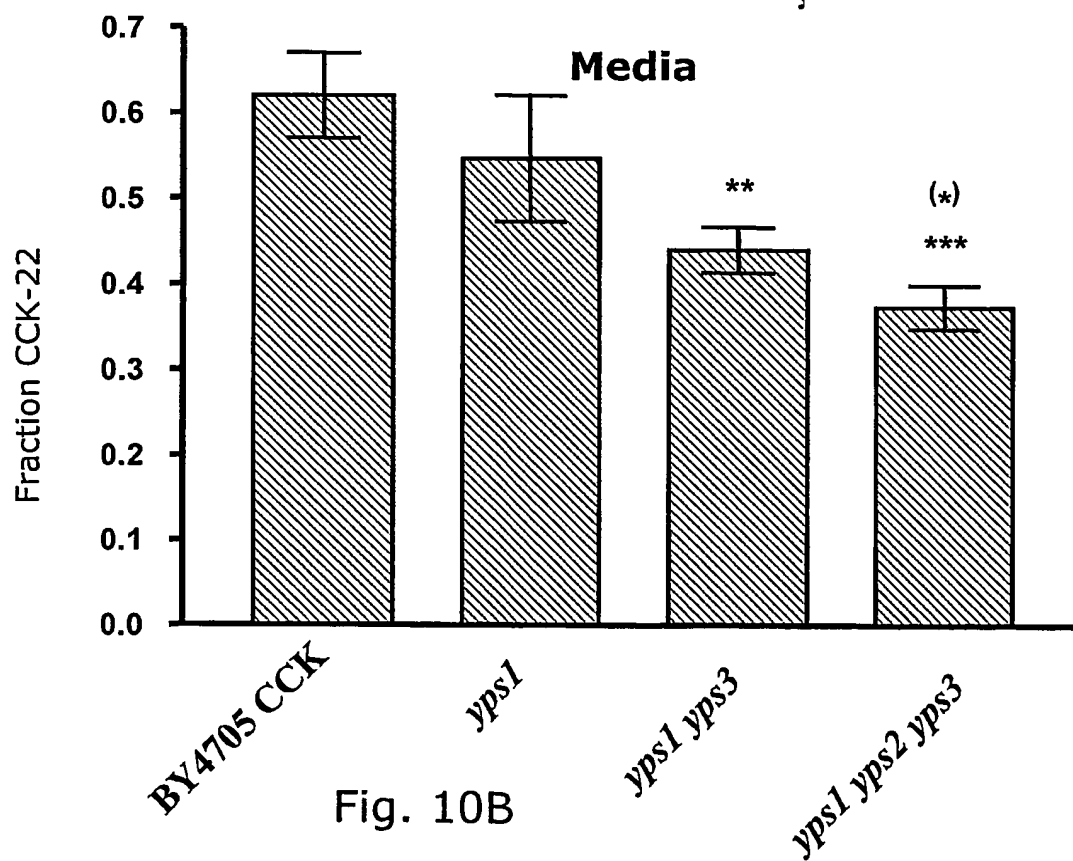
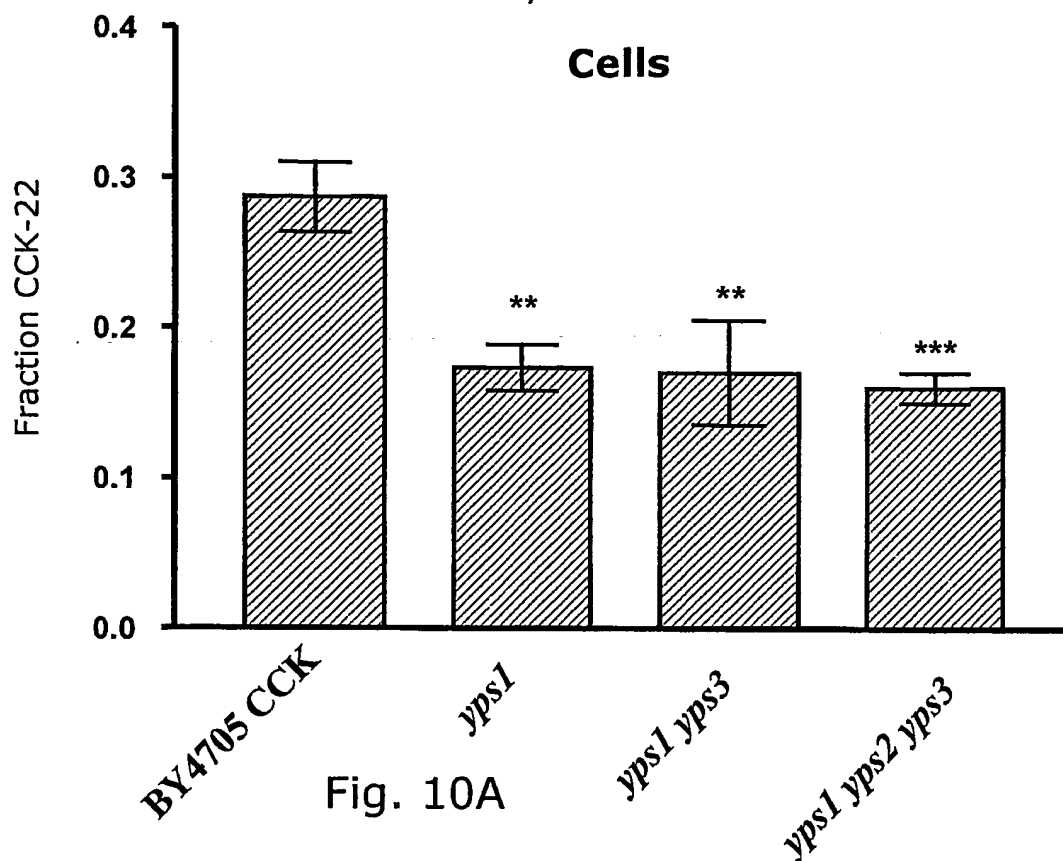
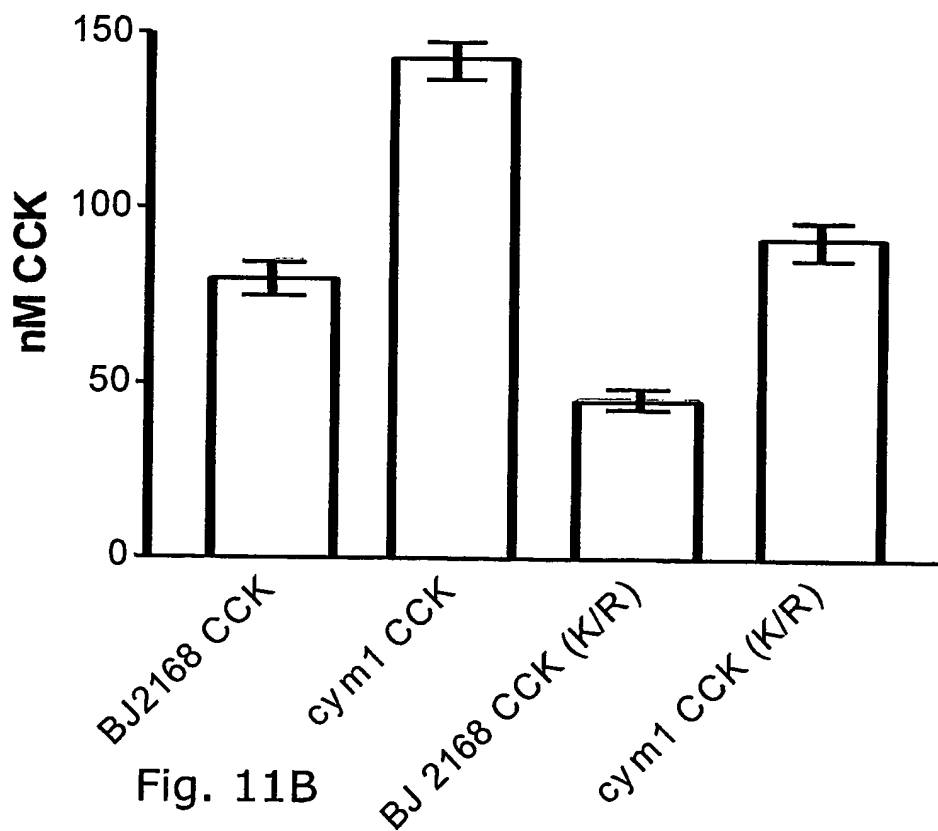
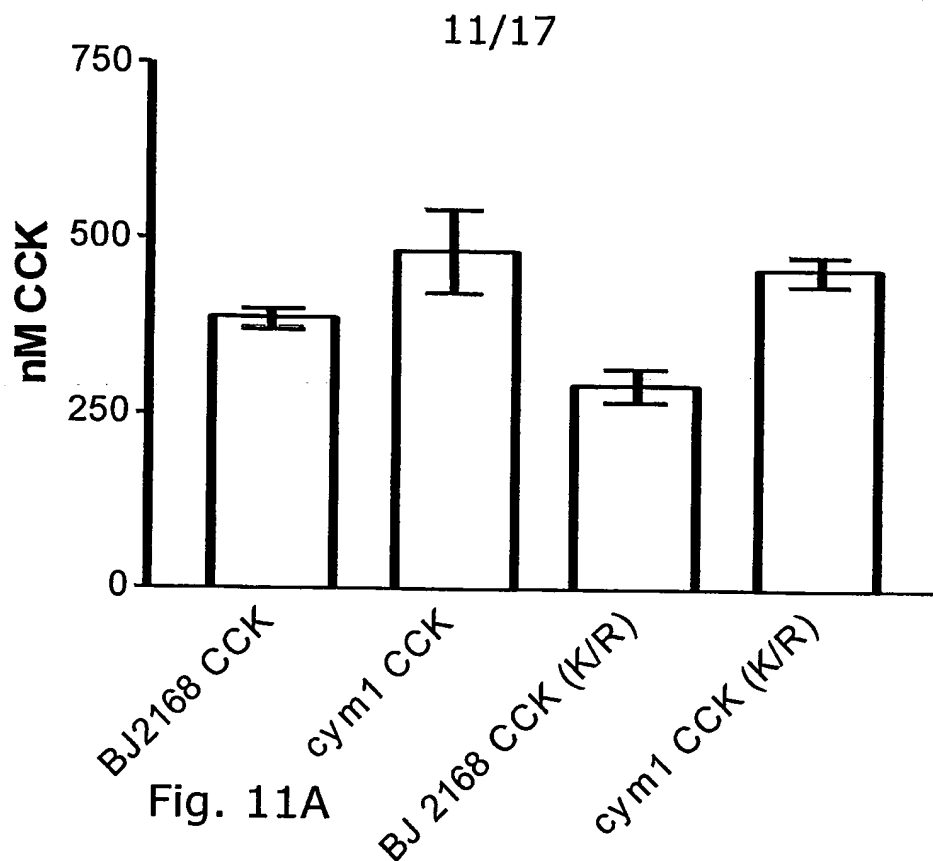


Fig. 9

10/17



603 8AM



800 84

10/528563

WO 2004/027067

PCT/DK2003/000609

12/17

ProCCK				Molecular mass		Strain	seq ID			
							NO:			
Prepromfalp // .SGLQRAEEAPRQLRV	CCK-61	CCK-58	CCK-39	CCK-22	CCK-8		43			
QLRVSQRTDGE				RAHLGALLAR	2433.3	2433.5	B	44		
VSQRTDGE				RAHLGALLAR	2036.1	2036.1	B	45		
YIQQARKAPSGRMSIV				KNLQNLDP	SHRISDRDYMGWMD	FGRRSAEEYEYPS	6051.9*	6051.6*	B	46
YIQQARKAPSGRMSIVK				1932.1	1932.2	A & B	47			
YIQQARKAPSGRMSIV				1805.2	1805.0	A	48			
NLQNLDP				SHRISD	1509.0	1508.7	A	49		
NLQNLDP				SHRISDRDYMGWMD	FG	2766.2	2766.1	A	50	
NLQNLDP				SHRISDRDYMGWMD	FGRRSAEEYEYPS	4133.8	4133.9	A & B	51	
DYMGWMD				FGRRSAEEYEYPS	2488.0	2488.1	A	52		

12/17

Fig. 12

13/17

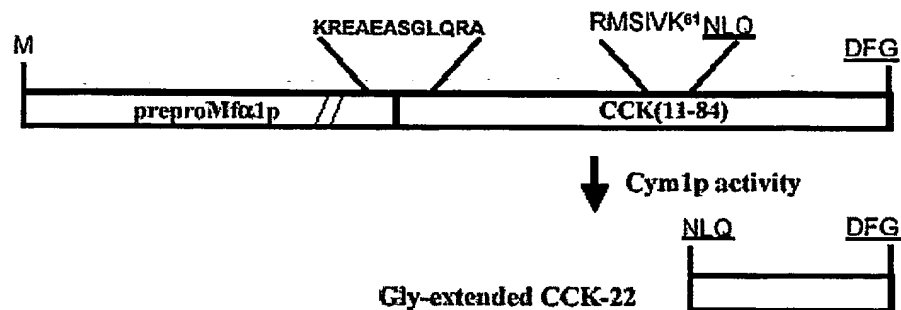


Fig. 13A

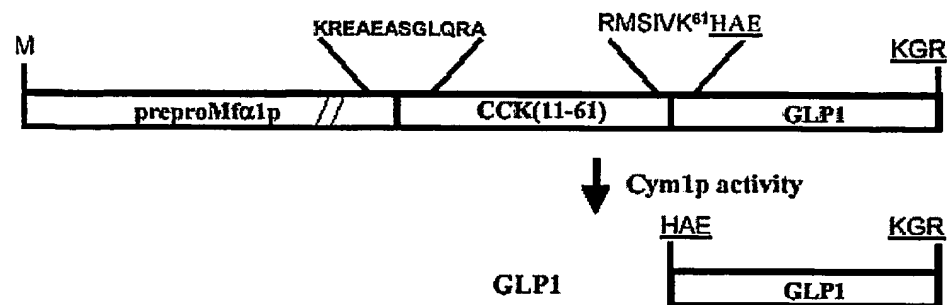


Fig. 13B

14/17

ATGAGATTTTCCTTCAATTTTTACTGCAGTTTTATTTCGCAGCATCCTCCGCATTAGCTGCT
1 -----+-----+-----+-----+-----+-----+-----+-----+ 60
TACTCTAAAGGAAGTTAAAAATGACGTCAAATAAGCGTCGTAGGAGGCGTAATCGACGA
M R F P S I F T A V L F A A S S A L A A -
CCAGTCAACACTACAACAGAAGATGAAACGGCACAAATTCGGGCTGAAGCTGTCATCGGT
61 -----+-----+-----+-----+-----+-----+-----+ 120
GGTCAGTTGTGATGTTGTCTTCTACTTTGCCGTGTTTAAGGCCGACTTCGACAGTAGCCA
P V N T T T E D E T A Q I P A E A V I G -
TACTTAGATTTAGAAGGGGATTTTCGATGTTGCTGTTTTGCCATTTTCCAACAGCACAAAT
121 -----+-----+-----+-----+-----+-----+-----+ 180
ATGAATCTAAATCTTCCCCTAAAGCTACAACGACAAAACGGTAAAAGGTTGTCGTGTTTA
Y L D L E G D F D V A V L P F S N S T N -
AACGGGTTATTGTTTATAAATACTACTATTGCCAGCATTTGCTGCTAAAGAAGAAGGGGTA
181 -----+-----+-----+-----+-----+-----+-----+ 240
TTGCCCAATAACAAATATTTATGATGATAACGGTCGTAACGACGATTTCTTCTTCCCAT
N G L L F I N T T I A S I A A K E E G V -
TCTTTGGATAAAAAGAGAGGCTGAAGCTCACCCGCTGGGCAGCCCCGGTTCAGCCTCGGAC
241 -----+-----+-----+-----+-----+-----+-----+ 300
AGAAACCTATTTTCTCTCCGACTTCGAGTGGGCGACCCGTCGGGGCCAAGTCGGAGCCTG
S L D K R E A E A H P L G S P G S A S D -
TTGGAACGTCGGGTTACAGGAGCAGCGCAACCATTTGCAGGGCAAATGTCGGAGCTG
301 -----+-----+-----+-----+-----+-----+-----+ 360
AACCTTTGCAGGCCCAATGTCTCGTCGCGTTGGTAAACGTCCCGTTTGACAGCCTCGAC
L E T S G L Q E Q R N H L Q G K L S E L -
CAGGTGGAGCAGACATCCCTGGAGCCCCCTCAGGAGAGCCCCGTCACAGGTGTCTGG
361 -----+-----+-----+-----+-----+-----+-----+ 420
GTCCACCTCGTCTGTAGGGACCTCGGGGAGGTCTCTCGGGGGCAGGGTGTCCACAGACC
Q V E Q T S L E P L Q E S P R P T G V W -
AAGTCCCGGGAGGTAGCCACCGAGGGCATCCGTGGGCACCGCAAATGGTCTCTACACC
421 -----+-----+-----+-----+-----+-----+-----+ 480
TTCAGGGCCCTCCATCGGTGGCTCCCGTAGGCACCCGTGGCGTTTTACCAGGAGATGTGG
K S R E V A T E G I R G H R K M V L Y T -
CTGCGGGCACCACGAAGCCCCAAGATGGTGCAAGGGTCTGGCTGCTTTGGGAGGAAGATG
481 -----+-----+-----+-----+-----+-----+-----+ 540
GACGCCCCTGGTGTCTCGGGGTTCTACCACGTTCCCGAGACCGACGAAACCCTCTTCTAC
L R A P R S P K M V Q G S G C F G R K M -
GACCGGATCAGCTCCTCCAGTGGCCTGGGCTGCAAAGTGCTGAGGCGGCATTAA
541 -----+-----+-----+-----+-----+-----+-----+ 594
CTGGCCTAGTCGAGGAGGTCACCGGACCCGACGTTTCACGACTCCGCCGTAATT
D R I S S S S G L G C K V L R R H * -

Fig. 14A

003 RAM 73 01911

Title: METHODS FOR INCREASING THE PRODUCTION OF A
RECOMBINANT POLYPEPTIDE FROM A HOST CELL
Inventor(s): Lars JONSON et al.
DOCKET NO.: 030307-0256

10/528563

WO 2004/027067

PCT/DK2003/000609

15/17

```
ATGAGATTTTCCTTCAATTTTTACTGCAGTTTTATTTCGCAGCATCCTCCGCATTAGCTGCT
1  -----+-----+-----+-----+-----+-----+-----+ 60
TACTCTAAAGGAAGTTAAAAATGACGTCAAATAAGCGTCGTAGGAGGCGTAATCGACGA

M R F P S I F T A V L F A A S S A L A A -

CCAGTCAACACTACAACAGAAGATGAAACGGCACAAATTCGGGCTGAAGCTGTCTATCGGT
61 -----+-----+-----+-----+-----+-----+-----+ 120
GGTCAGTTGTGATGTTGTCTTCTACTTTGCCGTGTTTAAGGCCGACTTCGACAGTAGCCA

P V N T T T E D E T A Q I P A E A V I G -

TACTTAGATTTAGAAGGGGATTTTCGATGTTGCTGTTTTGCCATTTTCCAACAGCACAAAT
121 -----+-----+-----+-----+-----+-----+-----+ 180
ATGAATCTAAATCTTCCCCTAAAGCTACAACGACAAAACGGTAAAAGGTTGTCTGTTTA

Y L D L E G D F D V A V L P F S N S T N -

AACGGGTTATTGTTTATAAAATACTACTATTGCCAGCATTGCTGCTAAAGAAGAAGGGGTA
181 -----+-----+-----+-----+-----+-----+-----+ 240
TTGCCCAATAACAAATATTTATGATGATAACGGTCGTAACGACGATTTCTTCTTCCCAT

N G L L F I N T T I A S I A A K E E G V -

TCTTTGGATAAAAGAGAGGCTGAAGCTAGCCCCAAGATGGTGCAAGGGTCTGGCTGCTTT
241 -----+-----+-----+-----+-----+-----+-----+ 300
AGAAACCTATTTTCTCTCCGACTTCGATCGGGGTTCTACCACGTTCCCAGACCGACGAAA

S L D K R E A E A S P K M V Q G S G C F -

GGGAGGAAGATGGACCGGATCAGCTCCTCCAGTGGCCTGGGCTGCAAAGTGCTGAGGCGG
301 -----+-----+-----+-----+-----+-----+-----+ 360
CCCTCCTTCTACCTGGCCTAGTCGAGGAGGTCACCGGACCCGACGTTTCACGACTCCGCC

G R K M D R I S S S S G L G C K V L R R -

CATTA
361 ----- 366
GTAATT

H * -
```

Fig. 14B

PAGE 10

10/528563

WO 2004/027067

CT/DK2003/000609

16/17

```
ATGAGATTTCTTCAATTTTTACTGCAGTTTTATTTCGCAGCATCCTCCGCATTAGCTGCT
1  -----+-----+-----+-----+-----+-----+ 60
TACTCTAAAGGAAGTTAAAAATGACGTCAAATAAGCGTCGTAGGAGGCGTAATCGACGA

M R F P S I F T A V L F A A S S A L A A -

CCAGTCAACACTACAACAGAAGATGAAACGGCACAAATTCGGGCTGAAGCTGTCATCGGT
61  -----+-----+-----+-----+-----+-----+ 120
GGTCAGTTGTGATGTTGTCTTCTACTTTGCCGTGTTTAAGGCCGACTTCGACAGTAGCCA

P V N T T T E D E T A Q I P A E A V I G -

TACTTAGATTTAGAAGGGGATTTTCGATGTTGCTGTTTTGCCATTTTCCAACAGCACAAAT
121 -----+-----+-----+-----+-----+-----+ 180
ATGAATCTAAATCTTCCCCTAAAGCTACAACGACAAAACGGTAAAAGGTTGTCGTGTTTA

Y L D L E G D F D V A V L P F S N S T N -

AACGGGTTATTGTTTATAAAATACTACTATTGCCAGCATTGCTGCTAAAGAAGAAGGGGTA
181 -----+-----+-----+-----+-----+-----+ 240
TTGCCCAATAACAAATATTTATGATGATAACGGTCGTAACGACGATTCTTCTTCCCCAT

N G L L F I N T T I A S I A A K E E G V -

TCTTTGGATAAAAGAAGCCCCAAGATGGTGCAAGGGTCTGGCTGCTTTGGGAGGAAGATG
241 -----+-----+-----+-----+-----+-----+ 300
AGAAACCTATTTTCTTCGGGGTTCTACCACGTTCACGACCGACGAAACCCTCCTTCTAC

S L D K R S P K M V Q G S G C F G R K M -

GACCGGATCAGCTCCTCCAGTGGCCTGGGCTGCAAAGTGCTGAGGCGGCATTAA
301 -----+-----+-----+-----+-----+-----+ 354
CTGGCCTAGTCGAGGAGGTCACCGGACCCGACGTTTCACGACTCCGCCGTAATT

D R I S S S S G L G C K V L R R H * -
```

Fig. 14C

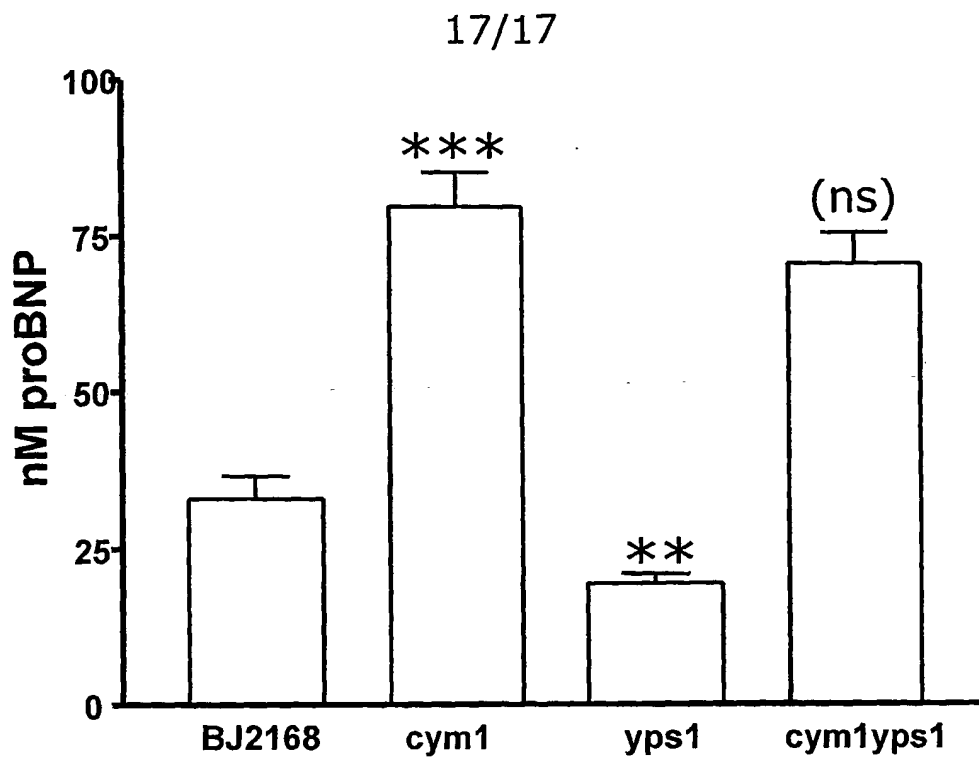


Fig. 15A

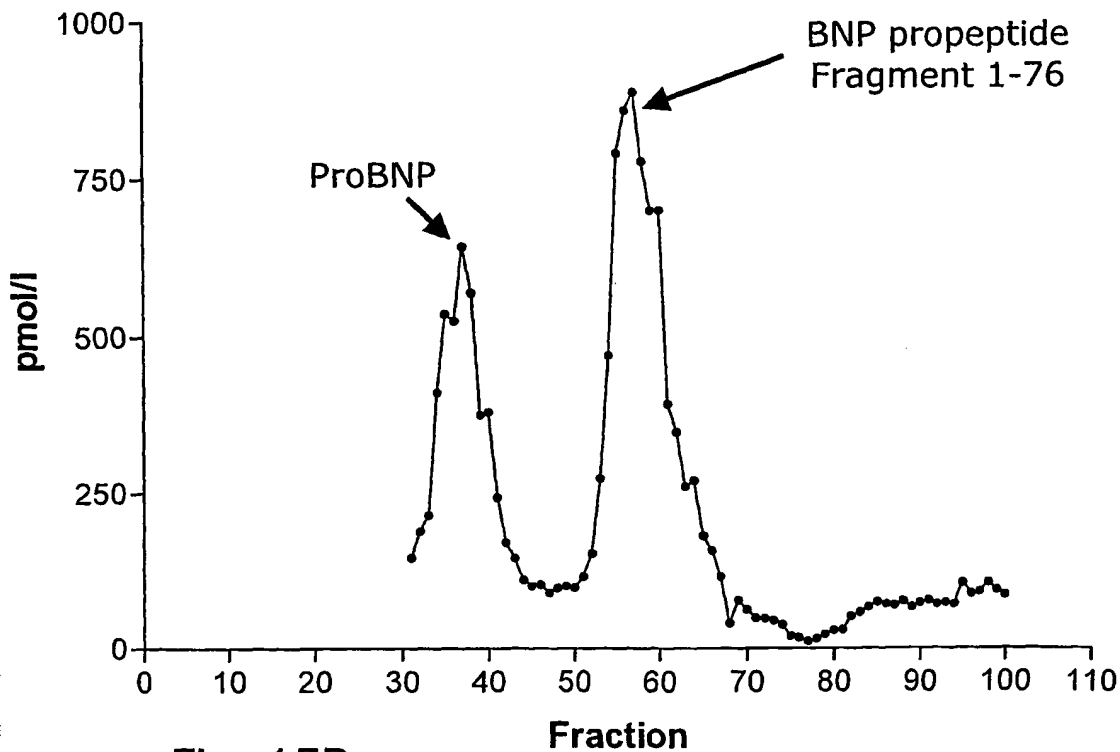


Fig. 15B